

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: NAKAMURA, SEIJI  
SAKURAI, TAKASHI  
NEZU, JUNI-ICHI
- (ii) TITLE OF INVENTION: GENE ENCODING ADSEVERIN
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
  - (B) STREET: P.O. Box 747
  - (C) CITY: Falls Church
  - (D) STATE: VA
  - (E) COUNTRY: USA
  - (F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: MURPHY Jr., Gerald M.
  - (B) REGISTRATION NUMBER: 28,977
  - (C) REFERENCE/DOCKET NUMBER: 230-110P
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 205-8000
  - (B) TELEFAX: (703) 205-8050

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Ala | His | Val | Lys | Gln | Ile | Pro | Phe | Asp | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Thr Asn Asp Leu Thr Ala Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Thr Asn Arg Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2418 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 27..2171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGCCGGAAC ATCGCGTGCC CGAGTC ATG GCC CAG GGG CTG TAC CAC GAG GAG 53  
Met Ala Gln Gly Leu Tyr His Glu Glu  
1 5

TTC GCC CGC GCG GGC AAG CGG GCG GGG CTG CAG GTC TGG AGA ATT GAG 101

|      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |     |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|
| Phe  | Ala | Arg | Ala | Gly | Lys | Arg | Ala | Gly | Leu | Gln | Val | Trp | Arg | Ile | Glu |  |  |     |
| 10   |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |  |  |     |
| AAG  | CTG | GAG | CTG | GTG | CCG | GTG | CCC | GAG | AGC | GCG | TAT | GGC | AAC | TTC | TAC |  |  | 149 |
| Lys  | Leu | Glu | Leu | Val | Pro | Val | Pro | Glu | Ser | Ala | Tyr | Gly | Asn | Phe | Tyr |  |  |     |
|      |     |     |     | 30  |     |     |     | 35  |     |     |     |     |     | 40  |     |  |  |     |
| GTC  | GGG | GAT | GCC | TAC | CTG | GTG | CTC | CAC | ACG | ACG | CAG | GCC | AGC | CGG | GGC |  |  | 197 |
| Val  | Gly | Asp | Ala | Tyr | Leu | Val | Leu | His | Thr | Thr | Gln | Ala | Ser | Arg | Gly |  |  |     |
|      |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |  |  |     |
| TTC  | ACC | TAC | CGC | CTG | CAC | TTC | TGG | CTG | GGA | AAG | GAG | TGT | ACT | CAG | GAT |  |  | 245 |
| Phe  | Thr | Tyr | Arg | Leu | His | Phe | Trp | Leu | Gly | Lys | Glu | Cys | Thr | Gln | Asp |  |  |     |
|      |     | 60  |     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |  |  |     |
| GAA  | AGC | ACA | GCA | GCT | GCC | ATC | TTT | ACT | GTT | CAG | ATG | GAT | GAC | TAT | TTG |  |  | 293 |
| Glu  | Ser | Thr | Ala | Ala | Ala | Ile | Phe | Thr | Val | Gln | Met | Asp | Asp | Tyr | Leu |  |  |     |
|      | 75  |     |     |     |     | 80  |     |     |     | 85  |     |     |     |     |     |  |  |     |
| GGT  | GGC | AAA | CCT | GTG | CAG | AAC | AGA | GAA | CTT | CAA | GGC | TAT | GAG | TCT | ACG |  |  | 341 |
| Gly  | Gly | Lys | Pro | Val | Gln | Asn | Arg | Glu | Leu | Gln | Gly | Tyr | Glu | Ser | Thr |  |  |     |
|      | 90  |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |  |     |
| GAT  | TTT | GTT | GGC | TAC | TTT | AAA | GGA | GGT | CTG | AAA | TAC | AAG | GCT | GGC | GGT |  |  | 389 |
| Asp  | Phe | Val | Gly | Tyr | Phe | Lys | Gly | Gly | Leu | Lys | Tyr | Lys | Ala | Gly | Gly |  |  |     |
|      |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |  |  |     |
| GTG  | GCG | TCT | GGA | CTC | AAT | CAT | GTG | CTT | ACA | AAT | GAC | TTG | ACT | GCT | CAG |  |  | 437 |
| Val  | Ala | Ser | Gly | Leu | Asn | His | Val | Leu | Thr | Asn | Asp | Leu | Thr | Ala | Gln |  |  |     |
|      |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |  |  |     |
| AGG  | CTC | CTG | CAT | GTG | AAA | GGT | CGG | AGA | GTC | GTC | AGG | GCC | ACG | GAA | GTT |  |  | 485 |
| Arg. | Leu | Leu | His | Val | Lys | Gly | Arg | Arg | Val | Val | Arg | Ala | Thr | Glu | Val |  |  |     |
|      |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |  |  |     |
| CCC  | CTA | AGC | TGG | GAC | AGT | TTC | AAC | AAG | GGT | GAC | TGC | TTC | ATC | ATT | GAC |  |  | 533 |
| Pro  | Leu | Ser | Trp | Asp | Ser | Phe | Asn | Lys | Gly | Asp | Cys | Phe | Ile | Ile | Asp |  |  |     |
|      |     | 155 |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     |  |  |     |
| CTT  | GGC | ACT | GAA | ATT | TAC | CAG | TGG | TGT | GGA | TCT | TCT | TGC | AAC | AAG | TAC |  |  | 581 |
| Leu  | Gly | Thr | Glu | Ile | Tyr | Gln | Trp | Cys | Gly | Ser | Ser | Cys | Asn | Lys | Tyr |  |  |     |
|      | 170 |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |  |  |     |
| GAG  | CGC | CTG | AAG | GCC | AGC | CAG | GTT | GCC | ATC | GGC | ATT | CGG | GAC | AAT | GAA |  |  | 629 |
| Glu  | Arg | Leu | Lys | Ala | Ser | Gln | Val | Ala | Ile | Gly | Ile | Arg | Asp | Asn | Glu |  |  |     |
|      |     |     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |  |  |     |
| AGG  | AAA | GGC | AGA | GCT | CAG | CTG | ATT | GTG | GTA | GAA | GAA | GGG | AGT | GAA | CCA |  |  | 677 |
| Arg  | Lys | Gly | Arg | Ala | Gln | Leu | Ile | Val | Val | Glu | Glu | Gly | Ser | Glu | Pro |  |  |     |
|      |     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |  |  |     |
| TCA  | GAG | CTT | ACA | AAG | GTA | TTA | GGG | GAA | AAG | CCA | AAG | CTT | AGG | GAT | GGA |  |  | 725 |
| Ser  | Glu | Leu | Thr | Lys | Val | Leu | Gly | Glu | Lys | Pro | Lys | Leu | Arg | Asp | Gly |  |  |     |
|      |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |  |  |     |
| GAA  | GAT | GAT | GAT | GAC | ATC | AAA | GCA | GAT | ATA | ACT | AAT | AGG | AAA | ATG | GCT |  |  | 773 |
| Glu  | Asp | Asp | Asp | Asp | Ile | Lys | Ala | Asp | Ile | Thr | Asn | Arg | Lys | Met | Ala |  |  |     |
|      | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     |  |  |     |
| AAA  | CTC | TAC | ATG | GTT | TCA | GAT | GCC | AGT | GGC | TCC | ATG | AAA | GTG | AGT | CTG |  |  | 821 |
| Lys  | Leu | Tyr | Met | Val | Ser | Asp | Ala | Ser | Gly | Ser | Met | Lys | Val | Ser | Leu |  |  |     |

|   |     |     |  |     |  |     |      |
|---|-----|-----|--|-----|--|-----|------|
| 250   |     | 255 |  | 260 |  | 265 |      |
| GTG GCA GAA GAA AAC CCC TTC TCC ATG GCG ATG CTT CTG TCT GAA GAA |     |     |  |     |  |     | 869  |
| Val Ala Glu Glu Asn Pro Phe Ser Met Ala Met Leu Leu Ser Glu Glu |     |     |  |     |  |     |      |
|   | 270 |     |  | 275 |  | 280 |      |
| TGC TTC ATT TTG GAC CAC GGT GCT GCA AAA CAG ATT TTT GTA TGG AAA |     |     |  |     |  |     | 917  |
| Cys Phe Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys |     |     |  |     |  |     |      |
|   | 285 |     |  | 290 |  | 295 |      |
| GGT AAA GAT GCT AAT CCC CAG GAG AGA AAG GCT GCC ATG AAG ACA GCT |     |     |  |     |  |     | 965  |
| Gly Lys Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala |     |     |  |     |  |     |      |
|   | 300 |     |  | 305 |  | 310 |      |
| GAG GAA TTC CTA CAG CAA ATG AAT TAT TCT ACG AAT ACC CAA ATT CAA |     |     |  |     |  |     | 1013 |
| Glu Glu Phe Leu Gln Gln Met Asn Tyr Ser Thr Asn Thr Gln Ile Gln |     |     |  |     |  |     |      |
|   | 315 |     |  | 320 |  | 325 |      |
| GTT CTT CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTC TTT AAG |     |     |  |     |  |     | 1061 |
| Val Leu Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys |     |     |  |     |  |     |      |
|   | 330 |     |  | 335 |  | 340 | 345  |
| GAC TGG AGA GAT AGA GAT CAG AGC GAT GGC TTC GGG AAA GTG TAT GTC |     |     |  |     |  |     | 1109 |
| Asp Trp Arg Asp Arg Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val |     |     |  |     |  |     |      |
|   | 350 |     |  | 355 |  | 360 |      |
| ACA GAA AAA GTG GCT CAC GTA AAA CAA ATT CCA TTT GAT GCC TCA AAA |     |     |  |     |  |     | 1157 |
| Thr Glu Lys Val Ala His Val Lys Gln Ile Pro Phe Asp Ala Ser Lys |     |     |  |     |  |     |      |
|   | 365 |     |  | 370 |  | 375 |      |
| TTG CAC AGC TCC CCA CAA ATG GCA GCC CAG CAT CAC GTG GTG GAT GAC |     |     |  |     |  |     | 1205 |
| Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val Asp Asp |     |     |  |     |  |     |      |
|   | 380 |     |  | 385 |  | 390 |      |
| GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT AGG GTC |     |     |  |     |  |     | 1253 |
| Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn Gly Arg Val |     |     |  |     |  |     |      |
|   | 395 |     |  | 400 |  | 405 |      |
| GAA ATT GAC CGA AAC TCG TAT GGT GAA TTC TAT GGT GGT GAT TGC TAC |     |     |  |     |  |     | 1301 |
| Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr |     |     |  |     |  |     |      |
|   | 410 |     |  | 415 |  | 420 | 425  |
| ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT ATC TAC ACC TGG CAA |     |     |  |     |  |     | 1349 |
| Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln |     |     |  |     |  |     |      |
|   | 430 |     |  | 435 |  | 440 |      |
| GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC CTG ACT |     |     |  |     |  |     | 1397 |
| Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe Leu Thr |     |     |  |     |  |     |      |
|   | 445 |     |  | 450 |  | 455 |      |
| GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG CAG ATT CGA GTC |     |     |  |     |  |     | 1445 |
| Val Gln Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Arg Val |     |     |  |     |  |     |      |
|   | 460 |     |  | 465 |  | 470 |      |
| TCC CAA GGC AAA GAA CCT GCT CAC CTG CTG AGT TTG TTC AAA GAC AAA |     |     |  |     |  |     | 1493 |
| Ser Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys Asp Lys |     |     |  |     |  |     |      |
|   | 475 |     |  | 480 |  | 485 |      |
| CCG CTC ATT ATT TAC AAG AAC GGA ACA TCA AAG AAA GAA GGT CAG GCA |     |     |  |     |  |     | 1541 |
| Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Glu Gly Gln Ala |     |     |  |     |  |     |      |
|   | 490 |     |  | 495 |  | 500 | 505  |

|   |      |
|---|------|
| CCA GCC CCC CCT ATA CGC CTC TTT CAA GTC CGA AGA AAC CTG GCT TCG<br>Pro Ala Pro Pro Ile Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser<br>510 515 520     | 1589 |
| ATC ACC AGA ATT ATG GAG GTA GAT GTT GAT GCA AAC TCA TTG AAT TCC<br>Ile Thr Arg Ile Met Glu Val Asp Val Asp Ala Asn Ser Leu Asn Ser<br>525 530 535     | 1637 |
| AAT GAT GTT TTT GTC CTG AAA CTG CGA CAA AAT AAT GGC TAC ATC TGG<br>Asn Asp Val Phe Val Leu Lys Leu Arg Gln Asn Asn Gly Tyr Ile Trp<br>540 545 550     | 1685 |
| ATA GGA AAA GGC TCC ACA CAG GAG GAG GAG AAA GGA GCA GAG TAC GTG<br>Ile Gly Lys Gly Ser Thr Gln Glu Glu Glu Lys Gly Ala Glu Tyr Val<br>555 560 565     | 1733 |
| GCA AGC GTC CTC AAA TGC AAA ACT TCG ACG ATT CAG GAA GGC AAG GAA<br>Ala Ser Val Leu Lys Cys Lys Thr Ser Thr Ile Gln Glu Gly Lys Glu<br>570 575 580 585 | 1781 |
| CCA GAG GAG TTT TGG AAT TCC CTT GGA GGG AAA AAA GAC TAC CAG ACC<br>Pro Glu Glu Phe Trp Asn Ser Leu Gly Gly Lys Lys Asp Tyr Gln Thr<br>590 595 600     | 1829 |
| TCT CCT CTG CTA GAA TCC CAG GCT GAA GAC CAT CCA CCT CGG CTT TAC<br>Ser Pro Leu Leu Glu Ser Gln Ala Glu Asp His Pro Pro Arg Leu Tyr<br>605 610 615     | 1877 |
| GGC TGC TCC AAC AAA ACT GGA AGA TTC ATT ATT GAA GAG GTT CCA GGA<br>Gly Cys Ser Asn Lys Thr Gly Arg Phe Ile Ile Glu Glu Val Pro Gly<br>620 625 630     | 1925 |
| GAG TTC ACC CAG GAT GAT TTA GCA GAA GAT GAT GTC ATG CTG TTA GAT<br>Glu Phe Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met Leu Leu Asp<br>635 640 645     | 1973 |
| GCT TGG GAA CAG ATT TTT ATT TGG ATT GGA AAA GAT GCC AAT GAA GTT<br>Ala Trp Glu Gln Ile Phe Ile Trp Ile Gly Lys Asp Ala Asn Glu Val<br>650 655 660 665 | 2021 |
| GAG AAA TCA GAA TCT CTG AAG TCT GCC AAA ATA TAC CTT GAG ACC GAC<br>Glu Lys Ser Glu Ser Leu Lys Ser Ala Lys Ile Tyr Leu Glu Thr Asp<br>670 675 680     | 2069 |
| CCT TCT GGA AGA GAC AAG AGG ACG CCA ATT GTC ATC ATA AAA CAG GGT<br>Pro Ser Gly Arg Asp Lys Arg Thr Pro Ile Val Ile Ile Lys Gln Gly<br>685 690 695     | 2117 |
| CAT GAG CCA CCT ACT TTC ACA GGC TGG TTC CTG GGC TGG GAT TCC AGC<br>His Glu Pro Pro Thr Phe Thr Gly Trp Phe Leu Gly Trp Asp Ser Ser<br>700 705 710     | 2165 |
| AGG TGG TAAACTGATT TTTGTAGGAA AAAACAAAT ATAATGGGGC AGCTGTCCCA<br>Arg Trp<br>715   | 2221 |
| GGGGGGAAGG AGGAGCTTGT TTAACTTTAG AAAATTAACC TCAGCCATAT GGCTATTTTT   | 2281 |
| CCGTGCTTAG AATTGTTTG AAATTTCTTT TAACTGGAA TTTTCTTATG TTAATATTTT   | 2341 |

TATAACTTTT CTTATGGACC AATATTAGCT CTGCTGGATG CTGACATATC TTTATATATG 2401  
 ACTTTTAAAA GGGGCCG 2418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 715 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Gln Gly Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Arg  
 1 5 10 15  
 Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val  
 20 25 30  
 Pro Glu Ser Ala Tyr Gly Asn Phe Tyr Val Gly Asp Ala Tyr Leu Val  
 35 40 45  
 Leu His Thr Thr Gln Ala Ser Arg Gly Phe Thr Tyr Arg Leu His Phe  
 50 55 60  
 Trp Leu Gly Lys Glu Cys Thr Gln Asp Glu Ser Thr Ala Ala Ala Ile  
 65 70 75 80  
 Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn  
 85 90 95  
 Arg Glu Leu Gln Gly Tyr Glu Ser Thr Asp Phe Val Gly Tyr Phe Lys  
 100 105 110  
 Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His  
 115 120 125  
 Val Leu Thr Asn Asp Leu Thr Ala Gln Arg Leu Leu His Val Lys Gly  
 130 135 140  
 Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe  
 145 150 155 160  
 Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln  
 165 170 175  
 Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Ser Gln  
 180 185 190  
 Val Ala Ile Gly Ile Arg Asp Asn Glu Arg Lys Gly Arg Ala Gln Leu  
 195 200 205  
 Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Thr Lys Val Leu  
 210 215 220  
 Gly Glu Lys Pro Lys Leu Arg Asp Gly Glu Asp Asp Asp Asp Ile Lys  
 225 230 235 240

Ala Asp Ile Thr Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp  
 245 250 255  
 Ala Ser Gly Ser Met Lys Val Ser Leu Val Ala Glu Glu Asn Pro Phe  
 260 265 270  
 Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe Ile Leu Asp His Gly  
 275 280 285  
 Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys Asp Ala Asn Pro Gln  
 290 295 300  
 Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu Phe Leu Gln Gln Met  
 305 310 315 320  
 Asn Tyr Ser Thr Asn Thr Gln Ile Gln Val Leu Pro Glu Gly Gly Glu  
 325 330 335  
 Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Arg Asp Arg Asp Gln  
 340 345 350  
 Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu Lys Val Ala His Val  
 355 360 365  
 Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His Ser Ser Pro Gln Met  
 370 375 380  
 Ala Ala Gln His His Val Val Asp Asp Gly Ser Gly Lys Val Gln Ile  
 385 390 395 400  
 Trp Arg Val Glu Asn Asn Gly Arg Val Glu Ile Asp Arg Asn Ser Tyr  
 405 410 415  
 Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro  
 420 425 430  
 Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala Asn Ala Thr Arg Asp  
 435 440 445  
 Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln Leu Asp Arg Ser Leu  
 450 455 460  
 Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln Gly Lys Glu Pro Ala  
 465 470 475 480  
 His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu Ile Ile Tyr Lys Asn  
 485 490 495  
 Gly Thr Ser Lys Lys Glu Gly Gln Ala Pro Ala Pro Pro Ile Arg Leu  
 500 505 510  
 Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr Arg Ile Met Glu Val  
 515 520 525  
 Asp Val Asp Ala Asn Ser Leu Asn Ser Asn Asp Val Phe Val Leu Lys  
 530 535 540  
 Leu Arg Gln Asn Asn Gly Tyr Ile Trp Ile Gly Lys Gly Ser Thr Gln  
 545 550 555 560  
 Glu Glu Glu Lys Gly Ala Glu Tyr Val Ala Ser Val Leu Lys Cys Lys

|             |   |  |     |  |     |
|-------------|---|--|-----|--|-----|
|             | 565   |  | 570 |  | 575 |
| Thr Ser Thr | Ile Gln Glu Gly Lys Glu Pro Glu Glu Phe Trp Asn Ser |  |     |  |     |
|             | 580   |  | 585 |  | 590 |
| Leu Gly Gly | Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Ser Gln |  |     |  |     |
|             | 595   |  | 600 |  | 605 |
| Ala Glu Asp | His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly |  |     |  |     |
|             | 610   |  | 615 |  | 620 |
| Arg Phe Ile | Ile Glu Glu Val Pro Gly Glu Phe Thr Gln Asp Asp Leu |  |     |  |     |
|             | 625   |  | 630 |  | 635 |
| Ala Glu Asp | Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile |  |     |  |     |
|             | 645   |  | 650 |  | 655 |
| Trp Ile Gly | Lys Asp Ala Asn Glu Val Glu Lys Ser Glu Ser Leu Lys |  |     |  |     |
|             | 660   |  | 665 |  | 670 |
| Ser Ala Lys | Ile Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg |  |     |  |     |
|             | 675   |  | 680 |  | 685 |
| Thr Pro Ile | Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr |  |     |  |     |
|             | 690   |  | 695 |  | 700 |
| Gly Trp Phe | Leu Gly Trp Asp Ser Ser Arg Trp                     |  |     |  |     |
|             | 705   |  | 710 |  | 715 |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 79..2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|  |     |
|--|-----|
| AAGGTTCTCTC CTGCTGCTCT CGGTTTAGTC CAAGATCAGC GATATCACGC GTCCCCCGGA | 60  |
| GCATCGCGTG CAGGAGCC ATG GCG CGG GAG CTA TAC CAC GAA GAG TTC GCC    | 111 |
| Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala                        |     |
| 1 5 10   |     |
| CGG GCG GGC AAG CAG GCG GGG CTG CAG GTC TGG AGG ATT GAG AAG CTG    | 159 |
| Arg Ala Gly Lys Gln Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu    |     |
| 15 20 25   |     |
| GAG CTG GTG CCC GTG CCC CAG AGC GCT CAC GGC GAC TTC TAC GTC GGG    | 207 |
| Glu Leu Val Pro Val Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly    |     |
| 30 35 40   |     |



|   |     |
|---|-----|
| GAT GCC TAC CTG GTG CTG CAC ACG GCC AAG ACG AGC CGA GGC TTC ACC<br>Asp Ala Tyr Leu Val Leu His Thr Ala Lys Thr Ser Arg Gly Phe Thr<br>45 50 55        | 255 |
| TAC CAC CTG CAC TTC TGG CTC GGA AAG GAG TGT TCC CAG GAT GAA AGC<br>Tyr His Leu His Phe Trp Leu Gly Lys Glu Cys Ser Gln Asp Glu Ser<br>60 65 70 75     | 303 |
| ACA GCT GCT GCC ATC TTC ACT GTT CAG ATG GAT GAC TAT TTG GGT GGC<br>Thr Ala Ala Ala Ile Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly<br>80 85 90        | 351 |
| AAG CCA GTG CAG AAT AGA GAA CTT CAA GGA TAT GAG TCT AAT GAC TTT<br>Lys Pro Val Gln Asn Arg Glu Leu Gln Gly Tyr Glu Ser Asn Asp Phe<br>95 100 105      | 399 |
| GTT AGC TAT TTC AAA GGC GGT CTG AAA TAC AAG GCT GGA GGC GTG GCA<br>Val Ser Tyr Phe Lys Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala<br>110 115 120     | 447 |
| TCT GGA TTA AAT CAT GTT CTT ACG AAC GAC CTG ACA GCC AAG AGG CTC<br>Ser Gly Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu<br>125 130 135     | 495 |
| CTA CAT GTG AAG GGT CGT AGA GTG GTG AGA GCC ACA GAA GTT CCC CTT<br>Leu His Val Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu<br>140 145 150 155 | 543 |
| AGC TGG GAC AGT TTC AAC AAG GGT GAC TGC TTC ATC ATT GAC CTT GGC<br>Ser Trp Asp Ser Phe Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly<br>160 165 170     | 591 |
| ACC GAA ATT TAT CAG TGG TGT GGT TCC TCG TGC AAC AAA TAT GAA CGT<br>Thr Glu Ile Tyr Gln Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg<br>175 180 185     | 639 |
| CTG AAG GCA AAC CAG GTA GCT ACT GGC ATT CGG TAC AAT GAA AGG AAA<br>Leu Lys Ala Asn Gln Val Ala Thr Gly Ile Arg Tyr Asn Glu Arg Lys<br>190 195 200     | 687 |
| GGA AGG TCT GAA CTA ATT GTC GTG GAA GAA GGA AGT GAA CCC TCA GAA<br>Gly Arg Ser Glu Leu Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu<br>205 210 215     | 735 |
| CTT ATA AAG GTC TTA GGG GAA AAG CCA GAG CTT CCA GAT GGA GGT GAT<br>Leu Ile Lys Val Leu Gly Glu Lys Pro Glu Leu Pro Asp Gly Gly Asp<br>220 225 230 235 | 783 |
| GAT GAT GAC ATT ATA GCA GAC ATA AGT AAC AGG AAA ATG GCT AAA CTA<br>Asp Asp Asp Ile Ile Ala Asp Ile Ser Asn Arg Lys Met Ala Lys Leu<br>240 245 250     | 831 |
| TAC ATG GTT TCA GAT GCA AGT GGC TCC ATG AGA GTG ACT GTG GTG GCA<br>Tyr Met Val Ser Asp Ala Ser Gly Ser Met Arg Val Thr Val Val Ala<br>255 260 265     | 879 |
| GAA GAA AAC CCC TTC TCA ATG GCA ATG CTG CTG TCT GAA GAA TGC TTT<br>Glu Glu Asn Pro Phe Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe<br>270 275 280     | 927 |

|   |      |
|---|------|
| ATT TTG GAC CAC GGG GCT GCC AAA CAA ATT TTC GTA TGG AAA GGT AAA<br>Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys<br>285 290 295     | 975  |
| GAT GCT AAT CCC CAA GAG AGG AAG GCT GCA ATG AAG ACA GCT GAA GAA<br>Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu<br>300 305 310 315 | 1023 |
| TTT CTA CAG CAA ATG AAT TAT TCC AAG AAT ACC CAA ATT CAA GTT CTT<br>Phe Leu Gln Gln Met Asn Tyr Ser Lys Asn Thr Gln Ile Gln Val Leu<br>320 325 330     | 1071 |
| CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTT TTT AAG GAC TGG<br>Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp<br>335 340 345     | 1119 |
| AGA GAT AAA GAT CAG AGT GAT GGC TTC GGG AAA GTT TAT GTC ACA GAG<br>Arg Asp Lys Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu<br>350 355 360     | 1167 |
| AAA GTG GCT CAA ATA AAA CAA ATT CCC TTT GAT GCC TCA AAA TTA CAC<br>Lys Val Ala Gln Ile Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His<br>365 370 375     | 1215 |
| AGT TCT CCG CAG ATG GCA GCC CAG CAC AAT ATG GTG GAT GAT GGT TCT<br>Ser Ser Pro Gln Met Ala Ala Gln His Asn Met Val Asp Asp Gly Ser<br>380 385 390 395 | 1263 |
| GGC AAA GTG GAG ATT TGG CGT GTA GAA AAC AAT GGT AGG ATC CAA GTT<br>Gly Lys Val Glu Ile Trp Arg Val Glu Asn Asn Gly Arg Ile Gln Val<br>400 405 410     | 1311 |
| GAC CAA AAC TCA TAT GGT GAA TTC TAT GGT GGT GAC TGC TAC ATC ATA<br>Asp Gln Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile<br>415 420 425     | 1359 |
| CTC TAC ACC TAT CCC AGA GGA CAG ATT ATC TAC ACG TGG CAA GGA GCA<br>Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala<br>430 435 440     | 1407 |
| AAT GCC ACA CGA GAT GAG CTG ACA ACA TCT GCG TTC CTG ACT GTT CAG<br>Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln<br>445 450 455     | 1455 |
| TTG GAT CGG TCC CTT GGA GGA CAG GCT GTG CAG ATC CGA GTC TCC CAA<br>Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln<br>460 465 470 475 | 1503 |
| GGC AAA GAG CCT GTT CAC CTA CTG AGT TTG TTC AAA GAC AAA CCG CTC<br>Gly Lys Glu Pro Val His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu<br>480 485 490     | 1551 |
| ATT ATT TAC AAG AAT GGA ACA TCA AAG AAA GGA GGT CAG GCA CCT GCT<br>Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Gly Gly Gln Ala Pro Ala<br>495 500 505     | 1599 |
| CCC CCT ACA CGC CTC TTT CAA GTC CGG AGA AAC CTG GCA TCT ATC ACC<br>Pro Pro Thr Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr<br>510 515 520     | 1647 |
| AGA ATT GTG GAG GTT GAT GTT GAT GCA AAT TCA CTG AAT TCT AAC GAT   | 1695 |

|             |             |            |            |            |            |            |     |     |     |     |     |     |     |     |     |      |  |
|-------------|-------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Arg         | Ile         | Val        | Glu        | Val        | Asp        | Val        | Asp | Ala | Asn | Ser | Leu | Asn | Ser | Asn | Asp |      |  |
| 525         |             |            |            |            |            | 530        |     |     |     |     | 535 |     |     |     |     |      |  |
| GTT         | TGT         | GTC        | CTG        | AAA        | CTG        | CCA        | CAA | AAT | AGT | GGC | TAC | ATC | TGG | GTA | GGA | 1743 |  |
| Val         | Cys         | Val        | Leu        | Lys        | Leu        | Pro        | Gln | Asn | Ser | Gly | Tyr | Ile | Trp | Val | Gly |      |  |
| 540         |             |            |            |            | 545        |            |     |     |     | 550 |     |     |     |     | 555 |      |  |
| AAA         | GGT         | GCT        | AGC        | CAG        | GAG        | GAG        | GAG | AAA | GGA | GCA | GAG | TAT | GTA | GCA | AGT | 1791 |  |
| Lys         | Gly         | Ala        | Ser        | Gln        | Glu        | Glu        | Glu | Lys | Gly | Ala | Glu | Tyr | Val | Ala | Ser |      |  |
|             |             |            |            | 560        |            |            |     |     | 565 |     |     |     |     | 570 |     |      |  |
| GTC         | CTA         | AAG        | TGC        | AAA        | ACC        | TTA        | AGG | ATC | CAA | GAA | GGC | GAG | GAG | CCA | GAG | 1839 |  |
| Val         | Leu         | Lys        | Cys        | Lys        | Thr        | Leu        | Arg | Ile | Gln | Glu | Gly | Glu | Glu | Pro | Glu |      |  |
|             |             |            | 575        |            |            |            |     | 580 |     |     |     |     |     | 585 |     |      |  |
| GAG         | TTC         | TGG        | AAT        | TCC        | CTT        | GGA        | GGG | AAA | AAA | GAC | TAC | CAG | ACC | TCA | CCA | 1887 |  |
| Glu         | Phe         | Trp        | Asn        | Ser        | Leu        | Gly        | Gly | Lys | Lys | Asp | Tyr | Gln | Thr | Ser | Pro |      |  |
|             |             | 590        |            |            |            |            | 595 |     |     |     |     | 600 |     |     |     |      |  |
| CTA         | CTG         | GAA        | ACC        | CAG        | GCT        | GAA        | GAC | CAT | CCA | CCT | CGG | CTT | TAC | GGC | TGC | 1935 |  |
| Leu         | Leu         | Glu        | Thr        | Gln        | Ala        | Glu        | Asp | His | Pro | Pro | Arg | Leu | Tyr | Gly | Cys |      |  |
|             |             | 605        |            |            |            | 610        |     |     |     |     | 615 |     |     |     |     |      |  |
| TCT         | AAC         | AAA        | ACT        | GGA        | AGA        | TTT        | GTT | ATT | GAA | GAG | ATT | CCA | GGA | GAG | TTC | 1983 |  |
| Ser         | Asn         | Lys        | Thr        | Gly        | Arg        | Phe        | Val | Ile | Glu | Glu | Ile | Pro | Gly | Glu | Phe |      |  |
|             |             | 620        |            |            | 625        |            |     |     |     | 630 |     |     |     |     | 635 |      |  |
| ACC         | CAG         | GAT        | GAT        | TTA        | GCT        | GAA        | GAT | GAT | GTC | ATG | TTA | CTA | GAT | GCT | TGG | 2031 |  |
| Thr         | Gln         | Asp        | Asp        | Leu        | Ala        | Glu        | Asp | Asp | Val | Met | Leu | Leu | Asp | Ala | Trp |      |  |
|             |             |            |            | 640        |            |            |     |     | 645 |     |     |     |     | 650 |     |      |  |
| GAA         | CAG         | ATA        | TTT        | ATT        | TGG        | ATT        | GGC | AAA | GAT | GCT | AAT | GAA | GTT | GAG | AAA | 2079 |  |
| Glu         | Gln         | Ile        | Phe        | Ile        | Trp        | Ile        | Gly | Lys | Asp | Ala | Asn | Glu | Val | Glu | Lys |      |  |
|             |             |            | 655        |            |            |            |     | 660 |     |     |     |     | 665 |     |     |      |  |
| AAA         | GAA         | TCT        | CTG        | AAG        | TCT        | GCC        | AAA | ATG | TAC | CTT | GAG | ACA | GAC | CCT | TCT | 2127 |  |
| Lys         | Glu         | Ser        | Leu        | Lys        | Ser        | Ala        | Lys | Met | Tyr | Leu | Glu | Thr | Asp | Pro | Ser |      |  |
|             |             | 670        |            |            |            |            | 675 |     |     |     |     | 680 |     |     |     |      |  |
| GGA         | AGA         | GAC        | AAG        | AGG        | ACA        | CCA        | ATT | GTC | ATC | ATA | AAA | CAG | GGC | CAT | GAG | 2175 |  |
| Gly         | Arg         | Asp        | Lys        | Arg        | Thr        | Pro        | Ile | Val | Ile | Ile | Lys | Gln | Gly | His | Glu |      |  |
|             |             | 685        |            |            |            | 690        |     |     |     |     | 695 |     |     |     |     |      |  |
| CCA         | CCC         | ACA        | TTC        | ACA        | GGC        | TGG        | TTC | CTG | GGC | TGG | GAT | TCC | AGC | AAG | TGG | 2223 |  |
| Pro         | Pro         | Thr        | Phe        | Thr        | Gly        | Trp        | Phe | Leu | Gly | Trp | Asp | Ser | Ser | Lys | Trp |      |  |
|             |             |            |            |            | 705        |            |     |     |     | 710 |     |     |     |     | 715 |      |  |
| TAAATTGGTA  | TTTGTA      | AAAAA      | GCAAACAAAC | ATTACAAGGC | AGTTATCTCA | TTGCTGTTTT |     |     |     |     |     |     |     |     |     | 2283 |  |
| GGGAGAGGAA  | CGGGAAAAAGC | TTTTTGCTTA | TTTGTCTTTT | GAAAATTAAG | GCTGGGCGCG |            |     |     |     |     |     |     |     |     |     | 2343 |  |
| GTGGCTCACA  | CCTGTAATCC  | CAGCACTTTG | AGAGGATGAG | GTAGGCGGAT | CACTGGGGTC |            |     |     |     |     |     |     |     |     |     | 2403 |  |
| AGGATTTCGA  | GACCAGCCTG  | GCCAACATGG | CGAAACCTCG | CCTCTACTAA | AAATACAAAA |            |     |     |     |     |     |     |     |     |     | 2463 |  |
| AAATTAGCTG  | CGCGTGGTGG  | TGCACGCCTG | TAGTCCCTGC | TACTTGAAG  | GCTGAGACAG |            |     |     |     |     |     |     |     |     |     | 2523 |  |
| GAAAAATTGCT | TGAGCCCAGG  | AGGCTGAGGT | TGCAGTGAGC | CAGGATTGCG | CCACCACACT |            |     |     |     |     |     |     |     |     |     | 2583 |  |
| CCAGCCTGGG  | CAACAGAGAC  | TCTGTCTCAA | AAAAAAAAAA | AAAAAAA    |            |            |     |     |     |     |     |     |     |     |     | 2630 |  |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Gln  
1 5 10 15  
Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val  
20 25 30  
Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly Asp Ala Tyr Leu Val  
35 40 45  
Leu His Thr Ala Lys Thr Ser Arg Gly Phe Thr Tyr His Leu His Phe  
50 55 60  
Trp Leu Gly Lys Glu Cys Ser Gln Asp Glu Ser Thr Ala Ala Ala Ile  
65 70 75 80  
Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn  
85 90 95  
Arg Glu Leu Gln Gly Tyr Glu Ser Asn Asp Phe Val Ser Tyr Phe Lys  
100 105 110  
Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His  
115 120 125  
Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His Val Lys Gly  
130 135 140  
Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe  
145 150 155 160  
Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln  
165 170 175  
Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Asn Gln  
180 185 190  
Val Ala Thr Gly Ile Arg Tyr Asn Glu Arg Lys Gly Arg Ser Glu Leu  
195 200 205  
Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Ile Lys Val Leu  
210 215 220  
Gly Glu Lys Pro Glu Leu Pro Asp Gly Gly Asp Asp Asp Asp Ile Ile  
225 230 235 240  
Ala Asp Ile Ser Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp  
245 250 255  
Ala Ser Gly Ser Met Arg Val Thr Val Val Ala Glu Glu Asn Pro Phe

| 260 |     |     |     |     |     |     |     |     |     | 265 |     |     |     |     |     |  |  |  |  | 270 |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| Ser | Met | Ala | Met | Leu | Leu | Ser | Glu | Glu | Cys | Phe | Ile | Leu | Asp | His | Gly |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Ala | Ala | Lys | Gln | Ile | Phe | Val | Trp | Lys | Gly | Lys | Asp | Ala | Asn | Pro | Gln |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Glu | Arg | Lys | Ala | Ala | Met | Lys | Thr | Ala | Glu | Glu | Phe | Leu | Gln | Gln | Met |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Asn | Tyr | Ser | Lys | Asn | Thr | Gln | Ile | Gln | Val | Leu | Pro | Glu | Gly | Gly | Glu |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Thr | Pro | Ile | Phe | Lys | Gln | Phe | Phe | Lys | Asp | Trp | Arg | Asp | Lys | Asp | Gln |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Ser | Asp | Gly | Phe | Gly | Lys | Val | Tyr | Val | Thr | Glu | Lys | Val | Ala | Gln | Ile |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Lys | Gln | Ile | Pro | Phe | Asp | Ala | Ser | Lys | Leu | His | Ser | Ser | Pro | Gln | Met |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Ala | Ala | Gln | His | Asn | Met | Val | Asp | Asp | Gly | Ser | Gly | Lys | Val | Glu | Ile |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Trp | Arg | Val | Glu | Asn | Asn | Gly | Arg | Ile | Gln | Val | Asp | Gln | Asn | Ser | Tyr |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Gly | Glu | Phe | Tyr | Gly | Gly | Asp | Cys | Tyr | Ile | Ile | Leu | Tyr | Thr | Tyr | Pro |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Arg | Gly | Gln | Ile | Ile | Tyr | Thr | Trp | Gln | Gly | Ala | Asn | Ala | Thr | Arg | Asp |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Glu | Leu | Thr | Thr | Ser | Ala | Phe | Leu | Thr | Val | Gln | Leu | Asp | Arg | Ser | Leu |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Gly | Gly | Gln | Ala | Val | Gln | Ile | Arg | Val | Ser | Gln | Gly | Lys | Glu | Pro | Val |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| His | Leu | Leu | Ser | Leu | Phe | Lys | Asp | Lys | Pro | Leu | Ile | Ile | Tyr | Lys | Asn |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Gly | Thr | Ser | Lys | Lys | Gly | Gly | Gln | Ala | Pro | Ala | Pro | Pro | Thr | Arg | Leu |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Phe | Gln | Val | Arg | Arg | Asn | Leu | Ala | Ser | Ile | Thr | Arg | Ile | Val | Glu | Val |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 515 |     |     |     | 520 |     |     |     |     |     | 525 |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Asp | Val | Asp | Ala | Asn | Ser | Leu | Asn | Ser | Asn | Asp | Val | Cys | Val | Leu | Lys |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 530 |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Leu | Pro | Gln | Asn | Ser | Gly | Tyr | Ile | Trp | Val | Gly | Lys | Gly | Ala | Ser | Gln |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Glu | Glu | Glu | Lys | Gly | Ala | Glu | Tyr | Val | Ala | Ser | Val | Leu | Lys | Cys | Lys |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Thr | Leu | Arg | Ile | Gln | Glu | Gly | Glu | Glu | Pro | Glu | Glu | Phe | Trp | Asn | Ser |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 580 |     |     |     | 585 |     |     |     |     |     | 590 |     |     |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |

Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Thr Gln  
 595 600 605  
 Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly  
 610 615 620  
 Arg Phe Val Ile Glu Glu Ile Pro Gly Glu Phe Thr Gln Asp Asp Leu  
 625 630 635 640  
 Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile  
 645 650 655  
 Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys Lys Glu Ser Leu Lys  
 660 665 670  
 Ser Ala Lys Met Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg  
 675 680 685  
 Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr  
 690 695 700  
 Gly Trp Phe Leu Gly Trp Asp Ser Ser Lys Trp  
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Val Tyr Val Thr Glu Lys Val Ala Gln Ile Lys Gln Ile Pro Phe

1

5

10

15

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 782 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu  
 1 5 10 15

Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg  
 20 25 30

Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg  
 35 40 45

Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys  
 50 55 60

Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro  
 65 70 75 80

Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val  
 85 90 95

Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu  
 100 105 110

His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala  
 115 120 125

Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val  
 130 135 140

Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr  
 145 150 155 160

Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe  
 165 170 175

Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val  
 180 185 190

Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu  
 195 200 205

Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile  
 210 215 220

His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala  
 225 230 235 240

Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala  
 245 250 255  
 Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln  
 260 265 270  
 Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala  
 275 280 285  
 Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser  
 290 295 300  
 Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro  
 305 310 315 320  
 Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His  
 325 330 335  
 Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr  
 340 345 350  
 Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys  
 355 360 365  
 Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly  
 370 375 380  
 Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp  
 385 390 395 400  
 Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn  
 405 410 415  
 Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala  
 420 425 430  
 Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln  
 435 440 445  
 Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr  
 450 455 460  
 Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr  
 465 470 475 480  
 Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala  
 485 490 495  
 Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln  
 500 505 510  
 Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln  
 515 520 525  
 Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met  
 530 535 540  
 Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro  
 545 550 555 560



Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr  
565 570 575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp  
580 585 590

Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr  
595 600 605

Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val  
610 615 620

Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly  
625 630 635 640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg  
645 650 655

Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys  
660 665 670

Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu  
675 680 685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp  
690 695 700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys  
705 710 715 720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala  
725 730 735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu  
740 745 750

Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp  
755 760 765

Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala  
770 775 780

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Lys Leu Ser Ala Gln Val Lys Gly Ser Leu Asn Ile Thr Thr  
1 5 10 15

Pro Gly Leu Gln Ile Trp Arg Ile Glu Ala Met Gln Met Val Pro Val

[illegible]

Asn Arg Thr Ser Gly Leu Gly Lys Thr His Thr Val Gly Ser Val Ala  
 355 360 365  
 Lys Val Glu Gln Val Lys Phe Asp Ala Thr Ser Met His Val Lys Pro  
 370 375 380  
 Gln Val Ala Ala Gln Gln Lys Met Val Asp Asp Gly Ser Gly Glu Val  
 385 390 395 400  
 Gln Val Trp Arg Ile Glu Asn Leu Glu Leu Val Pro Val Asp Ser Lys  
 405 410 415  
 Trp Leu Gly His Phe Tyr Gly Gly Asp Cys Tyr Leu Leu Leu Tyr Thr  
 420 425 430  
 Tyr Leu Ile Gly Glu Lys Gln His Tyr Leu Leu Tyr Val Trp Gln Gly  
 435 440 445  
 Ser Gln Ala Ser Gln Asp Glu Ile Thr Ala Ser Ala Tyr Gln Ala Val  
 450 455 460  
 Ile Leu Asp Gln Lys Tyr Asn Gly Glu Pro Val Gln Ile Arg Val Pro  
 465 470 475 480  
 Met Gly Lys Glu Pro Pro His Leu Met Ser Ile Phe Lys Gly Arg Met  
 485 490 495  
 Val Val Tyr Gln Gly Gly Thr Ser Arg Thr Asn Asn Leu Glu Thr Gly  
 500 505 510  
 Pro Ser Thr Arg Leu Phe Gln Val Gln Gly Thr Gly Ala Asn Asn Thr  
 515 520 525  
 Lys Ala Phe Glu Val Pro Ala Arg Ala Asn Phe Leu Asn Ser Asn Asp  
 530 535 540  
 Val Phe Val Leu Lys Thr Gln Ser Cys Cys Tyr Leu Trp Cys Gly Lys  
 545 550 555 560  
 Gly Cys Ser Gly Asp Glu Arg Glu Met Ala Lys Met Val Ala Asp Thr  
 565 570 575  
 Ile Ser Arg Thr Glu Lys Gln Val Val Val Glu Gly Gln Glu Pro Ala  
 580 585 590  
 Asn Phe Trp Met Ala Leu Gly Gly Lys Ala Pro Tyr Ala Asn Thr Lys  
 595 600 605  
 Arg Leu Gln Glu Glu Asn Leu Val Ile Thr Pro Arg Leu Phe Glu Cys  
 610 615 620  
 Ser Asn Lys Thr Gly Arg Phe Leu Ala Thr Glu Ile Pro Asp Phe Asn  
 625 630 635 640  
 Gln Asp Asp Leu Glu Glu Asp Asp Val Phe Leu Leu Asp Val Trp Asp  
 645 650 655  
 Gln Val Phe Phe Trp Ile Gly Lys His Ala Asn Glu Glu Glu Lys Lys  
 660 665 670

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Ala | Ala | Thr | Thr | Ala | Gln | Glu | Tyr | Leu | Lys | Thr | His | Pro | Ser | Gly |  |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |
| Arg | Asp | Pro | Glu | Thr | Pro | Ile | Ile | Val | Val | Lys | Gln | Gly | His | Glu | Pro |  |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |  |
| Pro | Thr | Phe | Thr | Gly | Trp | Phe | Leu | Ala | Trp | Asp | Pro | Phe | Lys | Trp | Ser |  |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |  |
| Asn | Thr | Lys | Ser | Tyr | Glu | Asp | Leu | Lys | Ala | Glu | Ser | Gly | Asn | Leu | Arg |  |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |  |
| Asp | Trp | Ser | Gln | Ile | Thr | Ala | Glu | Val | Thr | Ser | Pro | Lys | Val | Asp | Val |  |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |  |
| Phe | Asn | Ala | Asn | Ser | Asn | Leu | Ser | Ser | Gly | Pro | Leu | Pro | Ile | Phe | Pro |  |
|     |     | 755 |     |     |     | 760 |     |     |     |     |     | 765 |     |     |     |  |
| Leu | Glu | Gln | Leu | Val | Asn | Lys | Pro | Val | Glu | Glu | Leu | Pro | Glu | Gly | Val |  |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |
| Asp | Pro | Ser | Arg | Lys | Glu | Glu | His | Leu | Ser | Ile | Glu | Asp | Phe | Thr | Gln |  |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |  |
| Ala | Phe | Gly | Met | Thr | Pro | Ala | Ala | Phe | Ser | Ala | Leu | Pro | Arg | Trp | Lys |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |
| Gln | Gln | Asn | Leu | Lys | Lys | Glu | Lys | Gly | Leu | Phe |     |     |     |     |     |  |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATGCGGATC CAAYGAYYTN ACNGCNCA

28

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATGCATCGA TACRTGNGCN ACYTTYTC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCGAGGGTG GCGACGACTC C

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGGCCGCTT GACACCAGAC CAA

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAGCTATGAC CATGATTACG CCAA

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGACGGCCA GTGAATTGCG TAAT

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Ala | Lys | Val | Glu | Gln | Val | Lys | Phe | Asp | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |